In the Claims

1 (previously presented). A method of determining if active bioremediation activity is occurring at a site comprising:

a) contacting a microbial community at a subsurface site or down-well groundwater site with a sterilized solid support loaded or coated with an isotope enriched substrate;

b) incubating said solid support in said site for a period of time sufficient to establish a biofilm of microbes from said microbial community on said solid support;

c) identifying biomarkers obtained from the microbes on said solid support into which isotopes from said substrate have been incorporated; and

d) correlating the biomarkers containing isotopes from said substrate with particular microbes or subsets of microbial organisms known to cause bioremediation to determine if active bioremediation is occurring at said site.

2 (original). The method according to claim 1, wherein said biomarkers are selected from the group consisting of lipids, nucleic acids, proteins, and carbohydrates.

3 (previously presented). The method according to claim 1, wherein said biomarkers are respiratory quinones, diglycerides, sterols, intact phospholipids, poly beta-hydroxyalkonates, archaeol and caldarchaeols, ornithine lipids, sphingolipids, carotenoides, glycerides, glycolipids, gangliosides, eicosanoids, hopanes, isoprenoids, terpenes, fatty acids, fatty alcohols, waxes, fatty aldehydes, proteolipids or lysolipids.

4 (previously presented). The method according to claim 2, wherein said biomarkers are characteristic of a subset of microbial organisms.

5 (previously presented). The method according to claim 3, wherein said biomarkers are characteristic of a subset of microbial organisms.

6 (previously presented). The method according to claim 1, wherein $^{2}H$, $^{13}C$, $^{15}N$, an isotope of oxygen, or an isotope of sulfur is enriched in said substrate and incorporated into said biomarkers.

7 (canceled).

8 (currently amended). The method according to claim 1, wherein the biomarkers are identified by one or more of the following methods: pyrolysis, optionally with *in situ* derivatization and isotope ratio mass spectrometry, phospholipids fatty acid ~~(PFLA)~~(PLFA) analysis, polymerase chain reaction denaturing gradient gel electrophoresis (PCR-DGGE), expanded signature lipid biomarker analysis (SLB), terminal restriction fragment length polymorphism (T-RFLP) analysis of 16S rDNA or specific genes, high performance/atmospheric pressure chemical ionization/tandem mass spectrometry (HPLC/APCI/MS/MS) or liquid chromatography/tandem mass spectrometry (LC/MS/MS).

9 (previously presented). A method of identifying the microbial community at a site comprising:

a) contacting a microbial community at a subsurface site or down-well groundwater site with a sterilized solid support loaded or coated with an isotope enriched substrate;

b) incubating said solid support in said site for a period of time sufficient to establish a biofilm of microbes from said microbial community on said solid support;

c) identifying biomarkers obtained from the microbes on said solid support into which isotopes from said substrate have been incorporated; and

d) identifying the microbes present at said site by analyzing the biomarkers and associating isotope containing biomarkers with particular microbes or subsets of microbial organisms.

10 (original). The method according to claim 9, wherein said biomarkers are selected from the group consisting of lipids, nucleic acids, proteins, and carbohydrates.

11 (previously presented). The method according to claim 9, wherein said biomarkers are respiratory quinones, diglycerides, sterols, intact phospholipids, poly beta-hydroxyalkonates, archaeol and caldarchaeols, ornithine lipids, sphingolipids, carotenoides, glycerides, glycolipids, gangliosides, eicosanoids, hopanes, isoprenoids, terpenes, fatty acids, fatty alcohols, waxes, fatty aldehydes, proteolipids or lysolipids.

12 (previously presented). The method according to claim 10, wherein said biomarkers are characteristic of a subset of microbial organisms.

13 (previously presented). The method according to claim 11, wherein said biomarkers are characteristic of a subset of microbial organisms.

14 (previously presented). The method according to claim 9, wherein $^{2}H$, $^{13}C$, $^{15}N$, an isotope of oxygen, or an isotope of sulfur is enriched in said substrate and incorporated into said biomarkers.

15 (canceled).

16 (currently amended). The method according to claim 9 wherein the biomarkers are identified by one or more of the following methods: pyrolysis, optionally with *in situ* derivatization and isotope ratio mass spectrometry, phospholipids fatty acid ~~(PFLA)~~ (PLFA) analysis, polymerase chain reaction denaturing gradient gel electrophoresis (PCR-DGGE), expanded signature lipid biomarker analysis (SLB), terminal restriction fragment length polymorphism (T-RFLP) analysis of 16S rDNA or specific genes, high performance/atmospheric pressure chemical ionization/tandem mass spectrometry (HPLC/APCI/MS/MS) or liquid chromatography/tandem mass spectrometry (LC/MS/MS).

17 (previously presented). The method according to claim 1, wherein said site is a down-well groundwater site.

18 (previously presented). The method according to claim 1, wherein said site is a subsurface site.

19 (previously presented). The method according to claim 6, wherein $^{2}H$ or $^{15}N$ is enriched in said substrate and incorporated into said biomarkers.

20 (previously presented). The method according to claim 6, wherein $^{33}S$, $^{34}S$, or $^{36}S$ is enriched in said substrate and incorporated into said biomarkers.

21 (previously presented). The method according to claim 9, wherein said site is a down-well groundwater site.

22 (previously presented). The method according to claim 9, wherein said site is a subsurface site.

23 (previously presented). The method according to claim 14, wherein $^{2}H$, $^{15}N$, $^{33}S$, $^{34}S$, or $^{36}S$ is enriched in said substrate and incorporated into said biomarkers.

24 (canceled).

25 (previously presented). The method according to claim 1, wherein said sterile solid support comprises one or more perforated tube containing a solid support that is loaded or coated with a substrate.

26 (previously presented). The method according to claim 25, wherein said perforated tube contains a solid support loaded or coated with a substrate and said solid support is selected from glass beads, metal beads, thin strands of glass or metal, glass wool and/or polymeric beads.

27 (previously presented). The method according to claim 26, wherein said perforated tube is incubated in a site for a period of time sufficient to: establish a biofilm of microbes from a microbial community on said solid support; and allow for the incorporation of an isotope into a biomarker in said microbes.

28 (previously presented). The method according to claim 9, wherein said sterile solid support comprises one or more perforated tube containing a solid support that is loaded or coated with a substrate.

29 (previously presented). The method according to claim 28, wherein said perforated tube contains a solid support loaded or coated with a substrate and said solid support is selected from glass beads, metal beads, thin strands of glass or metal, glass wool and/or polymeric beads.

30 (previously presented). The method according to claim 29, wherein said perforated tube is incubated in a site for a period of time sufficient to: establish a biofilm of microbes from a microbial community on said solid support; and allow for the incorporation of an isotope into a biomarker in said microbes.

31 (previously presented). The method according to claim 1, wherein said isotope enriched substrate is an isotope enriched form of a contaminant present at the site.

32-33 (canceled).

34 (new). The method according to claim 1, wherein said isotope enriched substrate is a poyaromatic hydrocarbon, a tar, an asphaltene, a chlorobenzene, or a polychlorobiphenyl compound.